AMENDMENTS

In the Specification:

Please amend the paragraph on page 37, starting at line13 as follows:

The proteinase activities of *P. gingivalis* culture fractions were measured using the substrates N-tertiary-butoxycarbonyl-Ile-Glu-Gly-Arg-7-amido-4-methylcoumarin or N-tertiary-butoxy-carbonyl-Glu-Lys-Lys-7-amido-4-methylcoumarin at 30 C in Tris buffer without added reducing agents. Substrate hydrolysis was monitored over time by absorption at 460 nm using a 380 nm excitation beam on a ~~Perkin Elmer~~ PERKIN ELMER® LS 50B luminescence spectrophotometer.

Please amend the paragraph on page 39, starting at line 11 as follows:

Enzyme-linked immunosorbant assays (ELISA) were performed in polystyrene microtiter wells. Porphyrins and hemoglobin were used to coat the surfaces in 0.1 M NaOH or bicarbonate buffer pH 9 to determine optimal coating concentrations for saturation binding of rHA2. All wells were blocked and washed in PBS (2.7 mM KCl-1.5 mM KH_2PO_4-137 mM NaC1-8.1 mM Na_2HOP_4) with 10 mM NaN_3 and 0.1% Tween 20 (PBS/Tween). Dilutions of rHA2 in 50mM acetate buffer pH 5.5 containing 137 mM NaC1, 0.1% Tween and 10mM NaN_3 (Acetate/Tween) were incubated overnight before washingin PBS/Tween. Primary murine monoclonal antibody (VA1) was applied in PBS/Tween at a concentration of 0.5 μg/m1 for 1 hr at 37 C. Secondary goat anti-mouse antibodies conjugated with AP (Dako Corp.) were applied at a concentration of 1.1 μg/m1 for 1 hr at 37 C, and then AP activity was monitored at 414 nm by hydrolysis of the substrate 4-nitrophenylphosphate (Boehringer GmbH, Mannheim, Germany) in 5 mM Tris (pH9.5) by using a ~~Titertek Twinreader PLUS~~ TITERTEK TWINREADER PLUS® photometer (absorbance maximum of 3.0 ELISA units). Mean apparent dissociation constants (K_ds) were derived by solid-phase ELISA as previously described (51).

Please amend the paragraph on page 44 starting at line 7 as follows:

Using linear synthetic peptides, the epitope of mAb 5A1 was determined to be associated with the peptide ALNPDNYLISKDVTG <400>1 (K_d = 3.8 nM) which represents amino acids #1215-1229 of the translated Kgp within the HA2 domain (Figure 7, peptide #1). Dot blot analysis of PVDF membrane confirmed the unique immunoreactivity of this peptide with mAb 5A1. Similar results were obtained with peptide #3 (<400>8). A search of SwissProt database for the linear sequence of peptide #1 or ~~GenBank~~ GENBANK® database using the deduced nucleic acid sequence of this epitope resulted in no molecules with perfect homology to the peptide other than the gingipains and HagA, a large hemagglutinin with regions of identity to the entire HA2 domain.

Please amend the paragraph on page 46, starting at line 8 as follows:

All entries for proteins used in the porphyrin biosynthesis pathway that are listed in the Swiss-Prot database (Release 37.0) were searched with TBlastN against the available genomic data for the *P. gingivalis* genome (45). This search ~~comprized~~ comprised 257 eukaryotic, archaeal and prokaryotic protein sequences used in different pathways related to porphyrin biosynthesis. These are the standard enzymes in porphyrin biosythesis, alternative enzymes used by subsets of organisms, the enzymes of the C_4 and C_5 pathways for 5-aminolevinulic acid synthesis, and enzymes used in Vitamin B_{12} synthesis. Preliminary sequence data for *P. gingivalis* was obtained from The Institute of Genomic Research through the website at ~~http://www.tigr.org~~ www.tigr.org.